

EXHIBIT 4

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BLAST 2 sequences

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

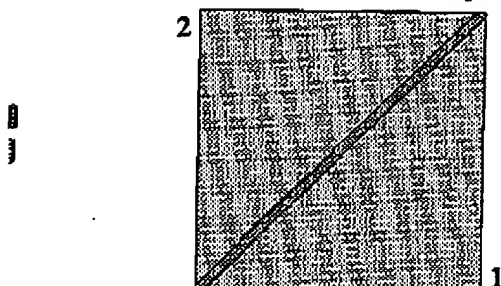
Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.00 wordsize: 3 Filter: ☒ Align

Sequence 1 lcl|7056_PATH9903

Length 222 (1 .. 222)

Sequence 2 gi|3916025

Hypothetical protein ymfC Length 217 (1 .. 217)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 380 bits (975), Expect = e-105
Identities = 185/216 (85%), Positives = 197/216 (90%)

Query: 3

MRQLITPENTMTKTSFRKHRVERFSSRQATRRTPEPQPTRVILENKPYPDVLFPQFTDEAGR
62MRQ I ENTM KTSFR H+V+RFSS+++TRR PE QPTRVILENKPYPDVLFPQFTDEAGR
Sbjct: 1 MRQFIISENTMQKTSFRNHQVKRFSSQRSTRKPEPQPTRVILENKPYPDVLFPQFTDEAGR
60Query: 63 STLKDFIPVQGVYAAGRLDRDSEGLLVLTNDGVLQARLTQPGKRTGKIYYVQVEGEPDDA
122TLK+FIPVQGVYAAGRLDRDSEGLLVLTN+G LQARLTQPGKRTGKIYYVQVEG P
Sbjct: 61 KTLKEFIPVQGVYAAGRLDRDSEGLLVLTNNGALQARLTQPGKRTGKIYYVQVEGIPTQD
120

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Query: 123 SLAKLRNGVTLNDGPTLPAGIERVNEPEWLWPRNPPIRERKSIPTSWLKITLYEGRNRQV
182

+L LRNGVTLNDGPTLPAG E V+EP WLWPRNPPIRERKSIPTSWLKITLYEGRNRQV

Sbjct: 121 ALEALRNGVTLNDGPTLPAGAELVDEPAWLWPRNPPIRERKSIPTSWLKITLYEGRNRQV
180

Query: 183 RRMTAHVGFPTRLRLIRYAMGSYTLDSLANGEWRDVT 218

RRMTAHVGFPTRLRLIRYAMG Y+LD+LANGWEVR+VT

Sbjct: 181 RRMTAHVGFPTRLRLIRYAMGDYSLDNLANGEWREVT 216

CPU time: 0.02 user secs. 0.02 sys. secs 0.03 total
secs.

| Lambda | K | H |
|--------|-------|-------|
| 0.318 | 0.136 | 0.407 |

Gapped

| Lambda | K | H |
|--------|--------|-------|
| 0.267 | 0.0410 | 0.140 |

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 542

Number of Sequences: 0

Number of extensions: 33

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 222

length of database: 181,542,687

effective HSP length: 111

effective length of query: 111

effective length of database: 90,771,438

effective search space: 10075629618

effective search space used: 10075629618

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.7 bits)

S2: 66 (30.0 bits)